



# SEQUENCE LISTING

<110> O'Brien, John S.

<120> METHODS FOR ALLEVIATING NEUROPATHIC PAIN

<130> 07256/024001

<140> 08/928,074

<141> 1997-09-11

<150> 08/611,307

<151> 1996-03-05

<150> PCT/US97/04143

<151> 1996-03-05

<160> 25

<170> PatentIn Ver. 2.0

<210> 1

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial peptide sequence

<400> 1

Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys  
1 5 10 15

Thr Glu Lys Glu Ile Leu  
20

<210> 2

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Peptide Sequence

<220>

<221> MOD\_RES

<222> (2)

<223> Ala at position 2 is a D-enantiomer

<400> 2

Thr Ala Leu Ile Asp Asn Asn Ala Thr Glu Glu Ile Leu Tyr  
1 5 10

<210> 3

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Peptide Sequence (Amino acids 18-29 of saposin C)

<400> 3  
Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu  
1 5 10

<210> 4  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (Mouse)

<400> 4  
Cys Gln Phe Val Met Asn Lys Phe Ser Glu Leu Ile Val Asn Asn Ala  
1 5 10 15  
Thr Glu Glu Leu Leu Tyr  
20

<210> 5  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (Rat)

<400> 5  
Cys Gln Leu Val Asn Arg Lys Leu Ser Glu Leu Ile Ile Asn Asn Ala  
1 5 10 15  
Thr Glu Glu Leu Leu  
20

<210> 6  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (Guinea Pig)

<400> 6  
Cys Glu Tyr Val Val Lys Lys Val Met Leu Leu Ile Asp Asn Asn Arg  
1 5 10 15  
Thr Glu Glu Lys Ile Ile  
20

<210> 7  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (Bovine)

<400> 7  
Cys Glu Phe Val Val Lys Glu Val Ala Lys Leu Ile Asp Asn Asn Arg  
1 5 10 15

Thr Glu Glu Glu Ile Leu  
20

<210> 8  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 8  
Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asp Asn Lys  
1 5 10 15

Thr Glu Lys Glu Ile Leu  
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<210> 9  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 9  
Thr Lys Leu Ile Asp Asn Asp Lys Thr Glu Lys Glu Ile Leu  
1 5 10

<210> 10  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 10  
Thr Lys Ser Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu  
1 5 10

<210> 11  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hCNTF)

<400> 11  
Tyr Val Lys His Gln Gly Leu Asn Lys Asn Ile Asn Leu Asp Ser Val

1

5

10

15

Asp Gly Val Pro  
20

<210> 12  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL-6)

<400> 12  
Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Gly  
1 5 10 15

<210> 13  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL-2)

<400> 13  
Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu  
1 5 10 15

Thr

<210> 14  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL-3)

<400> 14  
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu  
1 5 10

<210> 15  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL1-gamma)

<400> 15  
Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Thr Leu  
1 5 10

<210> 16  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hEPO)

<400> 16  
Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys  
1 5 10 15

Val

<210> 17  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 17  
Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys  
1 5 10 15

Ala Pro

<210> 18  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL-1beta)

<400> 18  
Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe Glu Ser Ala  
1 5 10 15

<210> 19  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hONC-M)

<400> 19  
Arg Pro Asn Ile Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu  
1 5 10 15

Leu

<210> 20  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 20  
Tyr Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu  
1 5 10 15

Ile Leu

<210> 21  
<211> 66  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Nucleic Acid Sequence

<220>  
<221> CDS  
<222> (1)..(66)

<400> 21  
tgt gaa ttc ctg gtg aag gag gtg acc aag ctg att gac aac aac aag 48  
Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys 15  
1 5 10 15

act gag aaa gaa ata ctc  
Thr Glu Lys Glu Ile Leu  
20 66

<210> 22  
<211> 2749  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(1572)

<400> 22  
atg tac gcc ctc ttc ctc ctg gcc agc ctc ctg ggc gcg gct cta gcc 48  
Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala 15  
1 5 10 15

ggc ccg gtc ctt gga ctg aaa gaa tgc acc agg ggc tcg gca gtg tgg 96  
Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp 30  
20

tgc cag aat gtg aag acg gcg tcc gac tgc ggg gca gtg aag cac tgc 144  
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys 45  
35 40

ctg cag acc gtt tgg aac aag cca aca gtg aaa tcc ctt ccc tgc gac 192  
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp

50

55

60

ata tgc aaa gac gtt gtc acc gca gct ggt gat atg ctg aag gac aat 240  
 ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn 80  
 65 70 75

gcc act gag gag gag atc ctt gtt tac ttg gag aag acc tgt gac tgg 288  
 Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp 95  
 85 90

ctt ccg aaa ccg aac atg tct gct tca tgc aag gag ata gtg gac tcc 336  
 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser 110  
 100 105

tac ctc cct gtc atc ctg gac atc att aaa gga gaa atg agc cgt cct 384  
 Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro 125  
 115 120

ggg gag gtg tgc tct gct ctc aac ctc tgc gag tct ctc cag aag cac 432  
 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His 140  
 130 135

cta gca gag ctg aat cac cag aag cag ctg gag tcc aat aag atc cca 480  
 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro 160  
 145 150 155

gag ctg gac atg act gag gtg gtg gcc ccc ttc atg gcc aac atc cct 528  
 Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro 175  
 165 170

ctc ctc ctc tac cct cag gac ggc ccc cgc agc aag ccc cag cca aag 576  
 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys 190  
 180 185

gat aat ggg gac gtt tgc cag gac tgc att cag atg gtg act gac atc 624  
 Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile 205  
 195 200

cag act gct gta cgg acc aac tcc acc ttt gtc cag gcc ttg gtg gaa 672  
 Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu 220  
 210 215

cat gtc aag gag gag tgt gac cgc ctg ggc cct ggc atg gcc gac ata 720  
 His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile 240  
 225 230 235

tgc aag aac tat atc agc cag tat tct gaa att gct atc cag atg atg 768  
 Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met 255  
 245 250

atg cac atg caa ccc aag gag atc tgt gcg ctg gtt ggg ttc tgt gat 816  
 Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp 270  
 260 265

gag gtg aaa gag atg ccc atg cag act ctg gtc ccc gcc aaa gtg gcc 864  
 Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala 285  
 275 280

tcc aag aat gtc atc cct gcc ctg gaa ctg gtg gag ccc att aag aag 912  
 Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys 300  
 290 295

cac gag gtc cca gca aag tct gat gtt tac tgt gag gtg tgt gaa ttc 960  
 His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe 320  
 305 310 315

ctg gtg aag gag gtg acc aag ctg att gac aac aac aag act gag aaa 1008  
 Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys  
 325 330 335

gaa ata ctc gac gct ttt gac aaa atg tgc tgc aag ctg ccg aag tcc 1056  
 Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser  
 340 345 350

ctg tgc gaa gag tgc cag gag gtg gtg gac acg tac ggc agc tcc atc 1104  
 Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile  
 355 360 365

ctg tcc atc ctg ctg gag gag gtc agc cct gag ctg gtg tgc agc atg 1152  
 Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met  
 370 375 380

ctg cac ctc tgc tct ggc acg cgg ctg cct gca ctg acc gtt cac gtg 1200  
 Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val  
 385 390 395 400

act cag cca aag gac ggt ggc ttc tgc gaa gtg tgc aag aag ctg gtg 1248  
 Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val  
 405 410 415

ggt tat ttg gat cgc aac ctg gag aaa aac agc acc aag cag gag atc 1296  
 Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile  
 420 425 430

ctg gct gct ctt gag aaa ggc tgc agc ttc ctg cca gac cct tac cag 1344  
 Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln  
 435 440 445

aag cag tgt gat cag ttt gtg gca gag tac gag ccc gtg ctg atc gag 1392  
 Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu  
 450 455 460

atc ctg gtg gag gtg atg gat cct tcc ttc gtg tgc ttg aaa att gga 1440  
 Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly  
 465 470 475 480

gcc tgc ccc tgc gcc cat aag ccc ttg ttg gga act gag aag tgt ata 1488  
 Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile  
 485 490 495

tgg ggc cca agc tac tgg tgc cag aac aca gag aca gca gcc cag tgc 1536  
 Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys  
 500 505 510

aat gct gtc gag cat tgc aaa cgc cat gtg tgg aac taggaggagg 1582  
 Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn  
 515 520

aatattccat cttggcagaa accacagcat tgggtttttt ctacttgtgt gtctggggga 1642

atgaacgcac agatctgttt gactttgtta taaaaatagg gctccccac ctccccatt 1702

tctgtgtcct ttattgtagc attgctgtct gcaagggagc ccctagcccc tggcagacat 1762

agctgcttca gtgccccctt tctctctgct agatggatgt tgatgcactg gaggtctttt 1822

agcctgccct tgcattggcg ctgctggagg aggagagagc tctgctggca tgagccacag 1882

tttcttgact ggaggccatc aaccctcttg gttgaggcct tgttctggcc ctgacatgtg 1942



cttgggcact ggtgggcctg ggcttctgag gtggcctcct gccctgatca gggaccctcc 2002  
 ccgctttcct gggcctctca gttgaacaaa gcagcaaaac aaaggcagtt ttatatgaaa 2062  
 gattagaagc ctggaataat caggctttttt aaatgatgta attccactg taatagcata 2122  
 gggatttttg aagcagctgc tgggtggcttg ggacatcagt ggggccaagg gttctctgtc 2182  
 cctggttcaa ctgtgatttg gctttcccgt gtctttcctg gtgatgcctt gtttgggggtt 2242  
 ctgtggggtt ggggtgggaag agggcaatct gcctgaatgt aacctgctag ctctccgaag 2302  
 gccctgcggg cctggccttg gtgagcgtgt ggacagtggg ggccgcgctg tgccctgctcg 2362  
 tgttgcctac atgtccctgg ctgttgaggc gctgcttcag cctgcacccc tcccttgctt 2422  
 catagatgct ccttttgacc ttttcaaata aatatggatg gcgagctcct aggcctctgg 2482  
 cttcctggta gagggcggca tgccgaaggg tctgctcggt gtggattgga tgctgggggtg 2542  
 tgggggttg aagctgtctg tggcccactt gggcacactt gggcacccac gcttctgtcc 2602  
 acttctgggt gccaggagac agcaagcaaa gccagcagga catgaagttg ctattaaatg 2662  
 gacttcgtga tttttgtttt gcactaaagt ttctgtgatt taacaataaa attctgttag 2722  
 ccagaaaaaa aaaaaaaaaa aaaaaaa 2749

<210> 23  
 <211> 524  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala  
 1 5 10 15  
 Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp  
 20 25 30  
 Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys  
 35 40 45  
 Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp  
 50 55 60  
 Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn  
 65 70 75 80  
 Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp  
 85 90 95  
 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser  
 100 105 110  
 Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro  
 115 120 125  
 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His  
 130 135 140  
 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro  
 145 150 155 160

Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro  
 165 170 175  
 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys  
 180 185 190  
 Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile  
 195 200 205  
 Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu  
 210 215 220  
 His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile  
 225 230 235 240  
 Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met  
 245 250 255  
 Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp  
 260 265 270  
 Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala  
 275 280 285  
 Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys  
 290 295 300  
 His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe  
 305 310 315 320  
 Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys  
 325 330 335  
 Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser  
 340 345 350  
 Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile  
 355 360 365  
 Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met  
 370 375 380  
 Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val  
 385 390 395 400  
 Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val  
 405 410 415  
 Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile  
 420 425 430  
 Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln  
 435 440 445  
 Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu  
 450 455 460  
 Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly  
 465 470 475 480  
 Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile  
 485 490 495  
 Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys  
 500 505 510

Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn  
515 520

<210> 24  
<211> 80  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 24  
Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr  
1 5 10 15  
Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe  
20 25 30  
Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln  
35 40 45  
Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu  
50 55 60  
Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly  
65 70 75 80

B'  
cont  
<210> 25  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<220>  
<221> PEPTIDE  
<222> (1)..(13)  
<223> X at position 4, 12 and 13 is any amino acid; X at  
position 7 is any amino acid, but not L or R; X at  
position 9 and 11 is a charged amino acid; and X  
at position 10, when present is a charged residue

<400> 25  
Leu Ile Arg Xaa Asn Asn Xaa Thr Xaa Xaa Xaa Xaa  
1 5 10